

[illegible]

aca aaa tgc ccc tgt cct gat ata gaa agg tca gcc ttt act gtg aag 193  
Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg Ser Ala Phe Thr Val Lys  
50 55 60

ctc	agt	gga	aaa	ctt	cct	ctt	cct	ttc	aag	ccc	atc	atc	ttc	aca	ggg	241
Leu	Ser	Gly	Lys	Leu	Pro	Leu	Pro	Phe	Lys	Pro	Ile	Ile	Phe	Thr	Gly	
65					70					75					80	
gtc	ctg	tac	aat	gcc	cag	agg	gat	tta	aag	gag	gcc	atg	gga	gtc	ttt	289
Val	Leu	Tyr	Asn	Ala	Gln	Arg	Asp	Leu	Lys	Glu	Ala	Met	Gly	Val	Phe	
				85					90					95		
gct	tgc	agg	gtg	cct	ggg	aat	tac	tac	tcc	agc	ttt	gat	gtt	gag	ctg	337
Ala	Cys	Arg	Val	Pro	Gly	Asn	Tyr	Tyr	Ser	Ser	Phe	Asp	Val	Glu	Leu	
			100					105					110			
cat	cat	tgc	aag	gtg	aat	att	tgg	cta	atg	agg	aag	caa	att	ttg	gct	385
His	His	Cys	Lys	Val	Asn	Ile	Trp	Leu	Met	Arg	Lys	Gln	Ile	Leu	Ala	
		115					120					125				
aat	aag	gaa	gaa	att	tct	aag	cag	caa	agc	att	caa	gag	gtg	act	tgg	433
Asn	Lys	Glu	Glu	Ile	Ser	Lys	Gln	Gln	Ser	Ile	Gln	Glu	Val	Thr	Trp	
	130					135					140					
gtg	ctg	tta	aag	gca	ttc	agt	ttc	ata	agg	gag	gca	gag	cat	aag	agt	481
Val	Leu	Leu	Lys	Ala	Phe	Ser	Phe	Ile	Arg	Glu	Ala	Glu	His	Lys	Ser	
145					150					155					160	
tca	gaa	aat	ttg	cac	cct	gac	aat	gtg	ata	aaa	aag	aaa	aac	cca	ttt	529
Ser	Glu	Asn	Leu	His	Pro	Asp	Asn	Val	Ile	Lys	Lys	Lys	Asn	Pro	Phe	
				165					170					175		
tct	gag	ggg	aaa	ttc	aag	ctg	gct	gca	gaa	att	tgc	ata	tgt	aat	gag	577
Ser	Glu	Gly	Lys	Phe	Lys	Leu	Ala	Ala	Glu	Ile	Cys	Ile	Cys	Asn	Glu	
			180					185					190			
gag	ctg	aat	gtt	aat	cct	caa	gac	aat	ggg	gaa	aat	atc	tcc	tgg	aca	625
Glu	Leu	Asn	Val	Asn	Pro	Gln	Asp	Asn	Gly	Glu	Asn	Ile	Ser	Trp	Thr	
		195					200					205				
tgt	cag	agg	tct	tca	cag	cag	tcc	atc	aaa	tca	ctg	gcc	tgg	agg	cct	673
Cys	Gln	Arg	Ser	Ser	Gln	Gln	Ser	Ile	Lys	Ser	Leu	Ala	Trp	Arg	Pro	
	210					215					220					
agg	aga	aaa	tgg	ttt	tgt	ggg	aca	ggc	cca	ggg	tcc	ctg	tgc	tgt	gtg	721

Arg 225	Arg	Lys	Trp	Phe	Cys 230	Gly	Thr	Gly	Pro	Gly 235	Ser	Leu	Cys	Cys	Val 240	
cag Gln	cct Pro	aga Arg	gac Asp	ttg Leu	gtg Val	ccc Pro	tgt Cys	gtc Val	cca Pro	gtt Val	aat Asn	tca Ser	gct Ala	gtg Val	gct Ala	769
tca Ser	gag Glu	ggg Gly	gca Ala	agc Ser	ccc Pro	aag Lys	cct Pro	tgg Trp	cag Gln	ctt Leu	cca Pro	agt Ser	ggg Gly	gtt Val	gag Glu	817
cct Pro	gtg Val	ggg Gly	gca Ala	aag Lys	aag Lys	tca Ser	aga Arg	att Ile	gag Glu	ggt Val	tgg Trp	gaa Glu	cct Pro	cca Pro	atc Ile	865
aga Arg	ttt Phe	cag Gln	aag Lys	ata Ile	tat Tyr	gga Gly	aac Asn	ccc Pro	tgg Trp	atg Met	ccc Pro	agg Arg	cag Gln	aag Lys	ttt Phe	913
gct Ala	gta Val	ggg Gly	gtg Val	ggg Gly	tcc Ser	tca Ser	tgg Trp	aga Arg	acc Thr	tct Ser	gca Ala	agg Arg	gta Val	gta Val	caa Gln	961
aag Lys	gga Gly	aat Asn	gtt Val	ggg Gly	tgg Trp	gag Glu	ccc Pro	cca Pro	cac His	aga Arg	gtc Val	ccc Pro	agt Ser	ggg Gly	gct Ala	1009
cca Pro	tct Ser	agt Ser	aga Arg	gct Ala	gtg Val	aga Arg	aga Arg	agt Ser	cca Pro	cca Pro	tcc Ser	tcc Ser	aga Arg	ctc Leu	cag Gln	1057
aag Lys	ggg Gly	aga Arg	tcc Ser	act Thr	gac Asp	agc Ser	ttg Leu	cag Gln	cat His	gtg Val	cct Pro	gaa Glu	aaa Lys	tcc Ser	aca Thr	1105
gac Asp	act Thr	cag Gln	tgc Cys	cag Gln	cct Pro	gtg Val	aaa Lys	gca Ala	gca Ala	ggg Gly	atg Met	gag Glu	tct Ser	gta Val	ccc Pro	1153
tac Tyr	aaa Lys	acc Thr	gta Val	gtg Val	gca Ala	gag Glu	ctg Leu	acc Thr	aag Lys	acc Thr	gtg Val	gga Gly	atc Ile	tac Tyr	ctc Leu	1201

Ile	Val	Val	Ile	Pro	Val	Leu	Ile	Thr	Ala	Val	Ile	Glu	His	Val	Glu
1				5					10					15	
Val	Ala	Gly	Pro	Pro	Ala	His	Pro	Arg	Pro	Pro	Glu	Glu	Val	Gly	Pro
			20					25					30		
Pro	Gly	Ala	Pro	Gly	Leu	Pro	Gln	Tyr	Thr	Gly	Glu	Ile	Ser	Glu	Met
		35					40					45			
Thr	Lys	Cys	Pro	Cys	Pro	Asp	Ile	Glu	Arg	Ser	Ala	Phe	Thr	Val	Lys
	50					55				60					
Leu	Ser	Gly	Lys	Leu	Pro	Leu	Pro	Phe	Lys	Pro	Ile	Ile	Phe	Thr	Gly
65					70				75						80
Val	Leu	Tyr	Asn	Ala	Gln	Arg	Asp	Leu	Lys	Glu	Ala	Met	Gly	Val	Phe
			85						90				95		
Ala	Cys	Arg	Val	Pro	Gly	Asn	Tyr	Tyr	Ser	Ser	Phe	Asp	Val	Glu	Leu
			100					105					110		
His	His	Cys	Lys	Val	Asn	Ile	Trp	Leu	Met	Arg	Lys	Gln	Ile	Leu	Ala
		115					120					125			
Asn	Lys	Glu	Glu	Ile	Ser	Lys	Gln	Gln	Ser	Ile	Gln	Glu	Val	Thr	Trp
	130					135				140					
Val	Leu	Leu	Lys	Ala	Phe	Ser	Phe	Ile	Arg	Glu	Ala	Glu	His	Lys	Ser
145					150					155					160

Ser Glu Asn Leu His Pro Asp Asn Val Ile Lys Lys Lys Asn Pro Phe  
 165 170 175  
 Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu Ile Cys Ile Cys Asn Glu  
 180 185 190  
 Glu Leu Asn Val Asn Pro Gln Asp Asn Gly Glu Asn Ile Ser Trp Thr  
 195 200 205  
 Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys Ser Leu Ala Trp Arg Pro  
 210 215 220  
 Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro Gly Ser Leu Cys Cys Val  
 225 230 235 240  
 Gln Pro Arg Asp Leu Val Pro Cys Val Pro Val Asn Ser Ala Val Ala  
 245 250 255  
 Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln Leu Pro Ser Gly Val Glu  
 260 265 270  
 Pro Val Gly Ala Lys Lys Ser Arg Ile Glu Val Trp Glu Pro Pro Ile  
 275 280 285  
 Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp Met Pro Arg Gln Lys Phe  
 290 295 300  
 Ala Val Gly Val Gly Ser Ser Trp Arg Thr Ser Ala Arg Val Val Gln  
 305 310 315 320  
 Lys Gly Asn Val Gly Trp Glu Pro Pro His Arg Val Pro Ser Gly Ala  
 325 330 335  
 Pro Ser Ser Arg Ala Val Arg Arg Ser Pro Pro Ser Ser Arg Leu Gln  
 340 345 350  
 Lys Gly Arg Ser Thr Asp Ser Leu Gln His Val Pro Glu Lys Ser Thr  
 355 360 365  
 Asp Thr Gln Cys Gln Pro Val Lys Ala Ala Gly Met Glu Ser Val Pro  
 370 375 380  
 Tyr Lys Thr Val Val Ala Glu Leu Thr Lys Thr Val Gly Ile Tyr Leu  
 385 390 395 400  
 Leu His Cys His Asp Leu Asp Val Arg His Gly Val Lys Arg Asp His  
 405 410 415  
 Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met  
 420 425 430  
 Gly Pro Val Pro Leu Cys Phe Gly Gln Phe Phe Pro Phe Gly Thr Ala  
 435 440 445  
 Val Phe Thr Gln Cys Leu Tyr Leu His Cys Met  
 450 455

<210> 3

<211> 1377

<212> DNA

<213> Artificial Sequence

<223> Degenerate polynucleotide encoding a polypeptide  
of SEQ ID NO:2

<222> (1)...(1377)

<223> Each  $n$  is independently A, T, G, or C.

<222> (1) ... (1377)

$\langle 223 \rangle$   $n = A, T, C$  or  $G$

athgtngtna	thccngtnyt	nathacngcn	gtathgarc	aygtngargt	ngcnggnccn	60
ccngcncayc	cnmgncncnc	ngargargtn	ggncncncng	gngcncncng	nytnccncar	120
tayacnggng	arathwsnga	ratgacnaar	tgyccntgyc	cngayathga	rmgnwsngcn	180
ttyacngtna	arytnwsngg	naarytnccn	ytnccnttya	arccnathat	httyacnggn	240
gtnytnaya	aygcncarmg	ngayytnaar	gargcnatgg	gngtnnttygc	ntgymngtn	300
ccnggnaayt	aytaywsnws	nttygaygtg	garytncayc	aytgyaargt	naayathtgg	360
ytnatgmnga	arcarathyt	ngcnaayaar	gargarathw	snaarcarca	rwsnathcar	420
gargtnacnt	gggtntytyt	naargcntty	wsnttyathm	gngargcnga	rcayaarwsn	480
wsngaraaay	tncaycenga	yaaygtath	aaraaraara	ayccnttyws	ngarggnaar	540
ttyaarytng	cngcngarat	htgyathtgy	aaygargary	tnaaygtnaa	yccncargay	600
aayggngara	ayathwsntg	gacntgycar	mgnwsnwsnc	arcarwsnat	haarwsnytn	660
gcntggmgnc	cnmgnmgnaa	rtggtytgy	ggnacnggnc	cnggnwsnyt	ntgytgygtg	720
carccnmng	ayytngtncc	ntgygtncn	gtnaaywsng	cngtnngcnws	ngarggngcn	780
wsnccnaarc	cntggcaryt	nccnwsnggn	gtngarccng	tnggngcnaa	raarwsnmgn	840
athgargtnt	gggarccnc	nathmgntty	caraaratht	ayggnaaycc	ntggatgccn	900
mgncaraart	tygcngtngg	ngtnggnwsn	wsntggmgna	cnwsngcnmg	ngtngtncar	960
aarggnaayg	tnggntggga	rcncncncay	mgngtnccnw	snggngcncc	nwsnwsnmgn	1020
gcngtnmgm	gnwsnccnc	nwsnwsnmgn	ytncaraarg	gnmgwnsnac	ngaywsnytn	1080
carcaygtnc	cngaraarws	nacngayacn	cartgycarc	cngtnaargc	ngcnggnatg	1140
garwsngtnc	cntayaarac	ngtngtngcn	garytnacna	aracngtngg	nathtayytn	1200
ytncaytgyc	aygayytnga	ygtnmgnca	ggngtnaarm	gngaycaytt	yggngcnytn	1260
mgnttygayt	gyccnacngg	nttymgnacn	tayatgggnc	cngtnccnyt	ntgyttyggg	1320
carttyttyc	cnttyggnac	ngcngtntty	acncartgyy	tntayytnca	ytgyatg	1377

<211> 31

### <213> Artificial Sequence

<223> Aromatic motif

 $\langle 222 \rangle \quad (2) \dots (6)$ 

<223> Each Xaa is any amino acid residue

 $\langle 222 \rangle \quad (7) \dots (7)$ 

<223> Xaa is asparagine or aspartic acid

$\langle 222 \rangle$  (8) ... (11)

<223> Each Xaa is independently any amino acid residue

 $\langle 222 \rangle \quad (12) \dots (12)$ 

<223> Xaa is phenylalanine, tyrosine, tryptophan, or leucine

$\langle 222 \rangle$  (13) ... (18)

<223> Each Xaa is independently any amino acid residue

<222> (20) ... (24)

<223> Each Xaa is independently any amino acid residue

 $\langle 222 \rangle \quad (26) \dots (26)$ 

<223> Xaa is any amino acid residue

<222> (28) . . . (31)

<223> Each Xaa is independently any amino acid residue

$\langle 400 \rangle$  4

Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 1 5 10 15  
 Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Xaa Xaa Xaa  
 20 25 30

<210> 5  
 <211> 1731  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(1731)

<400> 5

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Met	Leu	Ile	Glu	Ala	Tyr	Gly	Gly	Asp	Leu	Val	Ala	Gln	Gly	Ser	Lys	
1			5					10					15			

aaa	tgc	tgc	att	gga	gag	atg	ggg	tac	atg	cga	gtg	aca	atg	gga	aga	96
Lys	Cys	Cys	Ile	Gly	Glu	Met	Gly	Tyr	Met	Arg	Val	Thr	Met	Gly	Arg	
			20					25					30			

gtt	ggt	agc	tgg	aga	gaa	ctg	gga	aag	cct	tca	ggc	atc	tgg	gaa	atg	144
Val	Gly	Ser	Trp	Arg	Glu	Leu	Gly	Lys	Pro	Ser	Gly	Ile	Trp	Glu	Met	
		35					40					45				

gct	ggg	gat	aca	gag	gtg	aag	aag	aca	ggg	ttt	ctt	cag	gaa	ctc	act	192
Ala	Gly	Asp	Thr	Glu	Val	Lys	Lys	Thr	Gly	Phe	Leu	Gln	Glu	Leu	Thr	
	50					55					60					

ttc	cag	cag	gag	cct	ggc	atc	tcc	tcc	tct	cct	tct	tgc	tcc	cgc	tct	240
Phe	Gln	Gln	Glu	Pro	Gly	Ile	Ser	Ser	Ser	Pro	Ser	Cys	Ser	Arg	Ser	
65					70					75					80	

tgc	cat	gtg	aca	cca	cct	gct	cca	cct	gca	tct	tct	gcc	ata	att	gta	288
Cys	His	Val	Thr	Pro	Pro	Ala	Pro	Pro	Ala	Ser	Ser	Ala	Ile	Ile	Val	
				85					90					95		

aga	ttc	ctg	agg	ccc	tca	cca	gaa	gca	gat	gcc	agc	agc	atg	ctt	att	336
Arg	Phe	Leu	Arg	Pro	Ser	Pro	Glu	Ala	Asp	Ala	Ser	Ser	Met	Leu	Ile	
			100					105					110			

gca	cag	tct	gta	gaa	ccg	ata	gtg	gtc	ata	cct	gtc	tta	ata	acg	gca	384
Ala	Gln	Ser	Val	Glu	Pro	Ile	Val	Val	Ile	Pro	Val	Leu	Ile	Thr	Ala	
		115					120					125				

gtc	att	gag	cat	gta	gaa	gtt	gct	gga	cct	cca	gca	cac	ccc	agg	ccc	432
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099954660



Val	Ile	Glu	His	Val	Glu	Val	Ala	Gly	Pro	Pro	Ala	His	Pro	Arg	Pro	
130						135					140					
cca	gaa	gaa	gtg	ggg	cct	cct	ggt	gca	cca	ggt	tta	cca	caa	tat	aca	480
Pro	Glu	Glu	Val	Gly	Pro	Pro	Gly	Ala	Pro	Gly	Leu	Pro	Gln	Tyr	Thr	
145					150					155					160	
gga	gaa	ata	agt	gaa	atg	aca	aaa	tgc	ccc	tgt	cct	gat	ata	gaa	agg	528
Gly	Glu	Ile	Ser	Glu	Met	Thr	Lys	Cys	Pro	Cys	Pro	Asp	Ile	Glu	Arg	
				165					170						175	
tca	gcc	ttt	act	gtg	aag	ctc	agt	gga	aaa	ctt	cct	ctt	cct	ttc	aag	576
Ser	Ala	Phe	Thr	Val	Lys	Leu	Ser	Gly	Lys	Leu	Pro	Leu	Pro	Phe	Lys	
			180					185					190			
ccc	atc	atc	ttc	aca	ggg	gtc	ctg	tac	aat	gcc	cag	agg	gat	tta	aag	624
Pro	Ile	Ile	Phe	Thr	Gly	Val	Leu	Tyr	Asn	Ala	Gln	Arg	Asp	Leu	Lys	
		195				200						205				
gag	gcc	atg	gga	gtc	ttt	gct	tgc	agg	gtg	cct	ggg	aat	tac	tac	tcc	672
Glu	Ala	Met	Gly	Val	Phe	Ala	Cys	Arg	Val	Pro	Gly	Asn	Tyr	Tyr	Ser	
	210					215					220					
agc	ttt	gat	gtt	gag	ctg	cat	cat	tgc	aag	gtg	aat	att	tgg	cta	atg	720
Ser	Phe	Asp	Val	Glu	Leu	His	His	Cys	Lys	Val	Asn	Ile	Trp	Leu	Met	
225					230					235					240	
agg	aag	caa	att	ttg	gct	aat	aag	gaa	gaa	att	tct	aag	cag	caa	agc	768
Arg	Lys	Gln	Ile	Leu	Ala	Asn	Lys	Glu	Glu	Ile	Ser	Lys	Gln	Gln	Ser	
				245					250						255	
att	caa	gag	gtg	act	tgg	gtg	ctg	tta	aag	gca	ttc	agt	ttc	ata	agg	816
Ile	Gln	Glu	Val	Thr	Trp	Val	Leu	Leu	Lys	Ala	Phe	Ser	Phe	Ile	Arg	
			260					265					270			
gag	gca	gag	cat	aag	agt	tca	gaa	aat	ttg	cac	cct	gac	aat	gtg	ata	864
Glu	Ala	Glu	His	Lys	Ser	Ser	Glu	Asn	Leu	His	Pro	Asp	Asn	Val	Ile	
		275					280					285				
aaa	aag	aaa	aac	cca	ttt	tct	gag	ggg	aaa	ttc	aag	ctg	gct	gca	gaa	912
Lys	Lys	Lys	Asn	Pro	Phe	Ser	Glu	Gly	Lys	Phe	Lys	Leu	Ala	Ala	Glu	
	290					295					300					

att	tgc	ata	tgt	aat	gag	gag	ctg	aat	gtt	aat	cct	caa	gac	aat	ggg	960
Ile	Cys	Ile	Cys	Asn	Glu	Glu	Leu	Asn	Val	Asn	Pro	Gln	Asp	Asn	Gly	
305					310					315					320	
gaa	aat	atc	tcc	tgg	aca	tgt	cag	agg	tct	tca	cag	cag	tcc	atc	aaa	1008
Glu	Asn	Ile	Ser	Trp	Thr	Cys	Gln	Arg	Ser	Ser	Gln	Gln	Ser	Ile	Lys	
				325					330					335		
tca	ctg	gcc	tgg	agg	cct	agg	aga	aaa	tgg	ttt	tgt	ggg	aca	ggc	cca	1056
Ser	Leu	Ala	Trp	Arg	Pro	Arg	Arg	Lys	Trp	Phe	Cys	Gly	Thr	Gly	Pro	
			340					345					350			
ggg	tcc	ctg	tgc	tgt	gtg	cag	cct	aga	gac	ttg	gtg	ccc	tgt	gtc	cca	1104
Gly	Ser	Leu	Cys	Cys	Val	Gln	Pro	Arg	Asp	Leu	Val	Pro	Cys	Val	Pro	
		355					360					365				
gtt	aat	tca	gct	gtg	gct	tca	gag	ggc	gca	agc	ccc	aag	cct	tgg	cag	1152
Val	Asn	Ser	Ala	Val	Ala	Ser	Glu	Gly	Ala	Ser	Pro	Lys	Pro	Trp	Gln	
	370					375					380					
ctt	cca	agt	ggc	gtt	gag	cct	gtg	ggc	gca	aag	aag	tca	aga	att	gag	1200
Leu	Pro	Ser	Gly	Val	Glu	Pro	Val	Gly	Ala	Lys	Lys	Ser	Arg	Ile	Glu	
385					390					395					400	
gtt	tgg	gaa	cct	cca	atc	aga	ttt	cag	aag	ata	tat	gga	aac	ccc	tgg	1248
Val	Trp	Glu	Pro	Pro	Ile	Arg	Phe	Gln	Lys	Ile	Tyr	Gly	Asn	Pro	Trp	
			405						410					415		
atg	ccc	agg	cag	aag	ttt	gct	gta	ggg	gtg	ggg	tcc	tca	tgg	aga	acc	1296
Met	Pro	Arg	Gln	Lys	Phe	Ala	Val	Gly	Val	Gly	Ser	Ser	Trp	Arg	Thr	
			420					425					430			
tct	gca	agg	gta	gta	caa	aag	gga	aat	gtt	ggg	tgg	gag	ccc	cca	cac	1344
Ser	Ala	Arg	Val	Val	Gln	Lys	Gly	Asn	Val	Gly	Trp	Glu	Pro	Pro	His	
		435					440					445				
aga	gtc	ccc	agt	ggg	gct	cca	tct	agt	aga	gct	gtg	aga	aga	agt	cca	1392
Arg	Val	Pro	Ser	Gly	Ala	Pro	Ser	Ser	Arg	Ala	Val	Arg	Arg	Ser	Pro	
	450					455					460					
cca	tcc	tcc	aga	ctc	cag	aag	ggc	aga	tcc	act	gac	agc	ttg	cag	cat	1440

Pro Ser Ser Arg Leu Gln Lys Gly Arg Ser Thr Asp Ser Leu Gln His  
 465 470 475 480

gtg cct gaa aaa tcc aca gac act cag tgc cag cct gtg aaa gca gca 1488  
 Val Pro Glu Lys Ser Thr Asp Thr Gln Cys Gln Pro Val Lys Ala Ala  
 485 490 495

ggg atg gag tct gta ccc tac aaa acc gta gtg gca gag ctg acc aag 1536  
 Gly Met Glu Ser Val Pro Tyr Lys Thr Val Val Ala Glu Leu Thr Lys  
 500 505 510

acc gtg gga atc tac ctc ttg cat tgt cat gac ctg gac gtg aga cat 1584  
 Thr Val Gly Ile Tyr Leu Leu His Cys His Asp Leu Asp Val Arg His  
 515 520 525

gga gtc aaa aga gat cat ttt gga gct tta aga ttt gac tgc ccc act 1632  
 Gly Val Lys Arg Asp His Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr  
 530 535 540

gga ttt cgg act tat atg ggg ccc gta ccc ctt tgt ttt ggc caa ttt 1680  
 Gly Phe Arg Thr Tyr Met Gly Pro Val Pro Leu Cys Phe Gly Gln Phe  
 545 550 555 560

ttt cca ttt gga act gcc gta ttt acc caa tgc ctg tac ctc cat tgt 1728  
 Phe Pro Phe Gly Thr Ala Val Phe Thr Gln Cys Leu Tyr Leu His Cys  
 565 570 575

atg 1731  
 Met

&lt;210&gt; 6

&lt;211&gt; 577

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

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 1 5 10 15  
 Lys Cys Cys Ile Gly Glu Met Gly Tyr Met Arg Val Thr Met Gly Arg  
 20 25 30

F06671.092660



Val Asn Ser Ala Val Ala Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln  
 370 375 380  
 Leu Pro Ser Gly Val Glu Pro Val Gly Ala Lys Lys Ser Arg Ile Glu  
 385 390 395 400  
 Val Trp Glu Pro Pro Ile Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp  
 405 410 415  
 Met Pro Arg Gln Lys Phe Ala Val Gly Val Gly Ser Ser Trp Arg Thr  
 420 425 430  
 Ser Ala Arg Val Val Gln Lys Gly Asn Val Gly Trp Glu Pro Pro His  
 435 440 445  
 Arg Val Pro Ser Gly Ala Pro Ser Ser Arg Ala Val Arg Arg Ser Pro  
 450 455 460  
 Pro Ser Ser Arg Leu Gln Lys Gly Arg Ser Thr Asp Ser Leu Gln His  
 465 470 475 480  
 Val Pro Glu Lys Ser Thr Asp Thr Gln Cys Gln Pro Val Lys Ala Ala  
 485 490 495  
 Gly Met Glu Ser Val Pro Tyr Lys Thr Val Val Ala Glu Leu Thr Lys  
 500 505 510  
 Thr Val Gly Ile Tyr Leu Leu His Cys His Asp Leu Asp Val Arg His  
 515 520 525  
 Gly Val Lys Arg Asp His Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr  
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 Gly Phe Arg Thr Tyr Met Gly Pro Val Pro Leu Cys Phe Gly Gln Phe  
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